

Please cite:

```
/tmp/fastacAAygaWej: 995 aa
```

>SEQ ID NO:2

```
vs /tmp/fastaDAAzgaWej library
```

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searching /tmp/fastaDAAzgaWej library
```

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2

```
join: 39, opt: 27, gap-pen: -12/ -2, width: 16
```

Scan time: 0.034

The best scores are:

The best scores are: opt  
M13699 ACCESSION:M13699 NID: gi 180255 gb M13699. (1008) 2671

>>M13699 ACCESSION:M13699 NID: gi 180255 gb M13699.1 HUM (1008 aa)

```
initn: 1414 init1: 972 opt: 2671
```

Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

```

          10          20          30          40          50
SEQ      MKILILGIFLFLCSPGWAI DRHCYIGIEESIWNYPSPGKNMLNEKPFSEDL E---FLQ
          ::::::::::::::: . . : :::: . . :::: . . : : : : : : : :
M13699   MKILILGIFLFLCSTPAWAKEKHYYIGIIETTWDYA--SDHGEKKLISVDTEHSNIY LQ
          10          20          30          40          50

```

	60	70	80	90	100	110
SEQ	GGQARKSFVFKKALYFYQYTDNTFQRIIEKPSWLGFLGPMIKAETGDFIYVHVKNNASRAY					
	..	:	:	:	:	:
M13699	NGPDRIGRLYKKALYLQYTDETFRTTIEKPVWLGFLGPIIKAETGDKVYVHLKNLASRPY					
	60	70	80	90	100	110

	120	130	140	150	160	170
SEQ	SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKWYVEEHQGPSPDNCV					
	...	...	...	...	...	...
M13699	TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNVCV					
	120	130	140	150	160	170

	180	190	200	210	220	230
SEQ	TRIIYHSHIDTARDVASGLIGPILTCKRGTLNGDTEKDIDRSSFLMFSTTDESRSWYSDEN					
	.....	.....	..	..	:: ::	..... :: ::
M13699	TRIIYHSHIDAPKDIASGLIGPLIICKKDSL DKEKEKHIDREFVVMFSVVDENFSWYLEDN					
	180	190	200	210	220	230

	240	250	260	270	280	290
SEQ	IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPLNTMCAEDRVQWYFVGMGGVADIH					
	....	..	...	:	.....	....
M13699	IKTYCSEPEKVDKDNEFDQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFMGNEVDVH					
	240	250	260	270	280	290

```

      300      310      320      330      340      350
SEQ      PVYLRGQTLISRNHRKDTIMLFPSSEDAFMVAKAPGVWMLGCQ----IHESMQAFFKVS
      .....  :: :: :: :: :: :: :: :: :: :: :: :: :: :: .. :: :: :: ::
M13699  AAFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ
      300      310      320      330      340      350

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	360	370	380	390	400	410
SEQ	NCQKPST	EAFTGTH	VIHYIIA	AKEILWNY	APSGIDFF	TKKNLTAAGSKSQLFFERSPTR
	....	...	.	:	:	.....
M13699	ECNKSSSK	DNIRGKH	VRRHYIIA	AEIIWNY	APSGIDIFT	KENLTAPGSDSAVF
	EQGTTR					
	360	370	380	390	400	410
	420	430	440	450	460	
SEQ	IGGTYKK	LIYREYTD	ASFQTQKAR---	EEHLGILGP	VFKAEVGQTI	KITFYNNASLPLSI
	.....	...	:	:	.....	.....
M13699	IGGSYKK	LVYREYTD	ASF	TNRKERG	PEEEHLGILGP	VIWAEVGD
	TIRVTFH	NKGAYPLSI				
	420	430	440	450	460	470
	470	480	490	500	510	520
SEQ	QPPGLHY	NKSNEGLF	YETP	GGSTPP	SSHVSPGTT	FVYTWEV
	PKDVGPT	STDPNCL				
	.....	...	:	:	.....	.....
M13699	EPIGVRF	NKNNEG	TYISPNYN	PQSR	SVPPSASH	VAPTETFT
	TYEWTVP	KEVGPT	NADPVCL			
	480	490	500	510	520	530
	530	540	550	560	570	580
SEQ	TWFFYSS	VNGKKDIN	SGLLG	PLLICR	NGSLGDDG	KQKGV
	KEFYLL	ATIFDENE	SNLLDE			
	.....	...	:	:	.....	.....
M13699	AKMYSA	VDPTKDI	FTGLIG	PMKICK	KGSLHANG	RQKD
	VDKEFY	LFPTV	DENESL	LLED		
	540	550	560	570	580	590
	590	600	610	620	630	640
SEQ	N-RTFI	TEPENID	KEDTDC	QASNK	MY	SINGYMYGNL
	PGLD	TCLGDN	VLWHV	FSVGS	VEDL	
	.....	...	:	:	.....	.....
M13699	NIRMF	TTAPDQ	VDKEDE	FQESN	KMHSM	NGFM
	YGNQ	PGLT	MCKG	DSV	VWYLF	SAGNEAD
	600	610	620	630	640	650
	650	660	670	680	690	700
SEQ	HGIYF	SGNTFT	SLGARR	DTIP	MF	PYTSQ
	TLLMT	PDSIG	TFDL	VCMT	IKHNL	GGMKHKYHV
	.....	...	:	:	.....	.....
M13699	HGIYF	SGNTYL	WRGER	RD	TANL	FPQ
	TS	TLHM	WPD	TEG	TFN	VECL
	TTD	HYT	GGM	KQ	KYTV	
	660	670	680	690	700	710
	710	720	730	740	750	760
SEQ	RQCGK	PNPDQ	TQYQ	EKIIIT	IAA	EEM
	WDYS	PSR	KWEN	ELHHL	RREN	QTS
	SMY	VDR	SGTL			
	.....	...	:	:	.....	.....
M13699	NQCR	RQSE	DSTF	YLGERT	Y-IAA	VE
	WDYS	PQ	REWE	KELHHL	QEQNV	SN
	AF	LDK	GEFY			
	720	730	740	750	760	770
	770	780	790	800	810	820
SEQ	LGSKY	KKVLYR	QYDD	NFTN	QTKR	NEGEK
	HLDIL	GPLILL	NPGQ	IIQI	IFKN	KAAR
	PYSI					
	.....	...	:	:	.....	.....
M13699	IGSKY	KKVYR	QYTD	STFR	VP	VER
	KA	EEHL	GILGP	QLHAD	VGD	KVKI
	IFKN	MAT	R	PYSI		
	780	790	800	810	820	830
	830	840	850	860	870	880
SEQ	HAHGV	KTN	NSTV	VPTQ	PG	EIQI
	YT	WQIP	DR	TG	PTSL	DF
	ECIP	W	F	Y	STV	S
	VAK	DLH	SG	LV		
	.....	...	:	:	.....	.....
M13699	HAHGV	QTES	STV	TP	TL	P
	GET	LY	W	KIP	ERS	G
	AG	TED	SAC	IP	W	AY
	ST	V	D	Q	V	K
	DL	Y	S	G	L	I
	840	850	860	870	880	890

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      890      900      910      920      930
SEQ    GPLSVCR----KDINPN-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL
      ::: ::: : ::: .. : : : : : : : : : : : : : : : : : : : : : : :
M13699 GPLIVCRRPYLKVFNPRRKLEFALLFLVFDENESWYLDNKTYS DHPEKVNKDDEEFIE
      900      910      920      930      940      950

      940      950      960      970      980      990
SEQ    SNQMHAINGRLFGNNQGITFHVGDVVNWYLLIGIGNEADLHTVHFHGH SFYKHKYLI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M13699 SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGH SFQYKHR
      960      970      980      990      1000

```

995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:18:07 2002 done: Wed Sep 18 11:18:08 2002

Scan time: 0.034 Display time: 1.433

Function used was FASTA